For each of 27 traits, select independent SNPs.
Total: 2,190 unique markers

Annotate to RefSeq genes 1,410 genes

Merge into genetic blocks.

1,161 blocks

226 genes/blocks with several SNPs per region Check LD between these SNPs

Calculate
Brown score
for each gene in
each trait

FDR correction within a trait for gene score; significance level is 0.05/27 traits 378 genes have significant associations with more than two traits 175 of them are not listed at the previous stage, and have significant SNPs